IN THE CLAIMS:

1. (Previously Presented) A method for producing ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites comprising culturing organisms which have

a reduced Δ22-desaturase activity and

an increased HMG-CoA-reductase activity and

an increased activity of at least one of the activities selected from the group consisting of lanosterol C14-demethylase activity, squalene epoxidase activity and squalene synthetase activity

in comparison with the wild type.

2. (Previously presented) The method as claimed in claim 1, wherein, in order to reduce the Δ22-desaturase activity, the gene expression of a nucleic acid encoding a Δ22-desaturase is reduced in comparison with the wild type.

3. (Previously presented) The method as claimed in claim 2, wherein an organism without a functional Δ22-desaturase gene is used.

4. (Previously presented) The method as claimed in claim 1, wherein, in order to increase the HMG-CoA reductase activity, the gene expression of a nucleic acid encoding an HMG-CoA reductase is increased in comparison with the wild type.

5. (Previously presented) The method as claimed in claim 4, wherein, in order to increase gene expression, a nucleic acid construct comprising a nucleic acid encoding an HMG-CoA reductase is introduced into the organism and whose expression in the organism is subject to reduced regulation in comparison with the wild type.

6. (Previously presented) The method as claimed in claim 5, wherein the nucleic acid construct comprises a promoter which, in the organism, is subject to reduced regulation in comparison with the wild-type promoter.

7. (Previously presented) The method as claimed in claim 6, wherein the nucleic acid encoding an HMG-CoA reductase is a nucleic acid whose expression in the organism is subject to reduced regulation in comparison with the homologous, orthologous nucleic acid.

8. (Previously presented) The method as claimed in claim 7, wherein the nucleic acid encoding an HMG-CoA reductase is a nucleic acid which encodes the catalytic region of HMG-CoA reductase.

9. (Previously presented) The method as claimed in claim 8, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 4 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 4 at the amino acid level, which proteins have the enzymatic characteristic of an HMG-CoA reductase.

10. (Previously presented) The method as claimed in claim 9, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 3 is introduced.

11. (Previously presented) The method as claimed in any claim 1, wherein, in order to increase the lanosterol C 14-demethylase activity, the gene expression of a nucleic acid encoding a lanosterol C14-demethylase is increased in comparison with the wild type.

12. (Previously presented) The method as claimed in claim 11, wherein, in order to increase gene expression, one or more nucleic acids encoding a lanosterol C14-demethylase are introduced into the organism.

13. (Previously presented) The method as claimed in claim 12, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID.

NO. 6 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 6 at the amino acid level, which proteins have the enzymatic characteristic of a lanosterol C14-demethylase.

14. (Previously presented) The method as claimed in claim 13, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 5 is introduced.

15. (Previously presented) The method as claimed in claim 1, wherein, in order to increase the squalene epoxidase activity, the gene expression of a nucleic acid encoding a squalene epoxidase is increased in comparison with the wild type.

16. (Previously presented) The method as claimed in claim 15, wherein, in order to increase gene expression, one or more nucleic acids encoding a squalene epoxidase are introduced into the organism.

17. (Previously presented) The method as claimed in claim 16, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 8 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 8 at the amino acid level, which proteins have the enzymatic characteristic of a squalene epoxidase.

18. (Previously presented) The method as claimed in claim 17, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 7 is introduced.

19. (Previously presented) The method as claimed in claim 1, wherein, in order to increase the squalene synthetase activity, the gene expression of a nucleic acid encoding a squalene synthetase is increased in comparison with the wild type.

20. (Previously presented) The method as claimed in claim 19, wherein, in order to increase gene expression, one or more nucleic acids encoding a squalene synthetase are introduced into the organism.

21. (Previously presented) The method as claimed in claim 20, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 10 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 10 at the amino acid level, which proteins have the enzymatic characteristic of a squalene synthetase.

22. (Previously presented) The method as claimed in claim 21, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 9 is introduced.

23. (Previously presented) The method as claimed in claim 1, wherein the organism used is yeast.

24. (Previously presented) The method as claimed in claim 1, wherein, after the cultivation, the organism is harvested and ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites are subsequently isolated from the organism.

25. (Original) A genetically modified organism, where the genetic modification

reduces the Δ22-desaturase activity and

increases the HMG-CoA reductase activity and

increases at least one of the activities selected from the group consisting of lano-sterol C 14-demethylase activity, squalene epoxidase activity and squalene synthetase activity

in comparison with the wild type.

26. (Previously presented) The genetically modified organism as claimed in claim 25, where the genetic modification

reduces the Δ22-desaturase activity and

increases the HMG-CoA reductase activity and

increases the lanosterol C 14-demethylase activity

in comparison with the wild type.

27. (Previously presented) The genetically modified organism as claimed in claim 25, wherein the genetically modified organism has an increased content in ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites in comparison with the wild type.

28. (Previously presented) The genetically modified organism as claimed in claim 25, wherein the organism used is yeast.

29. (Previously presented) A method for the production of ergosta-5, 7-dienol and/or its biosynthetic intermediates and/or metabolites comprising culturing the genetically modified organism as claimed in claim 25.

30. (Original) A method for the generation of a genetically modified organism in which, starting from a starting organism,

the Δ22-desaturase activity is reduced and

the HMG-CoA reductase activity is increased and

at least one of the activities selected from the group consisting of lanosterol C14-demethylase activity, squalene epoxidase activity and squalene synthetase activity is increased.